Hayes

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

ENTERED

```
 1                            SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANT: Fox, Gary M
 6                       Jing, Shuqian
 7                       Wen, Duanzhi
 8
 9       (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
10
11      (iii) NUMBER OF SEQUENCES: 44
12
13       (iv) CORRESPONDENCE ADDRESS:
14            (A) ADDRESSEE: AMGEN INC
15            (B) STREET: One Amgen Center Drive
16            (C) CITY: Thousand Oaks
17            (D) STATE: CA
18            (E) COUNTRY: US
19            (F) ZIP: 91320-1789
20
21        (v) COMPUTER READABLE FORM:
22            (A) MEDIUM TYPE: Floppy disk
23            (B) COMPUTER: IBM PC compatible
24            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27       (vi) CURRENT APPLICATION DATA:
28            (A) APPLICATION NUMBER: US 08/866,354
29            (B) FILING DATE: 30-MAY-1997
30            (C) CLASSIFICATION:
31
32      (vii) PRIOR APPLICATION DATA:
33            (A) APPLICATION NUMBER: US 08/837,199
34            (B) FILING DATE: 14-APR-1997
35
36      (vii) PRIOR APPLICATION DATA:
37            (A) APPLICATION NUMBER: US 60/015,907
38            (B) FILING DATE: 22-APR-1996
39
40      (vii) PRIOR APPLICATION DATA:
41            (A) APPLICATION NUMBER: US 60/017,221
42            (B) FILING DATE: 09-MAY-1996
43
44     (viii) ATTORNEY/AGENT INFORMATION:
45            (A) NAME: Curry, Daniel R.
46            (B) REGISTRATION NUMBER: 32,727
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47                 (C) REFERENCE/DOCKET NUMBER: A-401B
48
49
50     (2) INFORMATION FOR SEQ ID NO:1:
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52          (i) SEQUENCE CHARACTERISTICS:
53               (A) LENGTH: 2568 base pairs
54               (B) TYPE: nucleic acid
55               (C) STRANDEDNESS: single
56               (D) TOPOLOGY: linear
57
58          (ii) MOLECULE TYPE: cDNA
59
60
61          (ix) FEATURE:
62               (A) NAME/KEY: CDS
63               (B) LOCATION: 540..1934
64
65
66          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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68     AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA        60
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70     CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG       120
71
72     CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA       180
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74     AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG       240
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76     TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT       300
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78     CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG       360
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80     CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT       420
81
82     TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA       480
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84     GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC        539
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86     ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC        587
87     Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
88      1               5                  10                  15
89
90     CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC        635
91     Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
92              20                  25                  30
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94     AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG        683
95     Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
96          35                  40                  45
97
98     CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC        731
99     L u Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/866,354*

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TIME: 14:49:34

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106    CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG      827
107    Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
108                            85                      90                  95
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110    AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA      875
111    Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
112                    100                     105                 110
113
114    AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG      923
115    Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
116                115                     120                 125
117
118    TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA      971
119    Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
120            130                     135                 140
121
122    GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC      1019
123    Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
124    145                     150                     155                 160
125
126    TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC      1067
127    Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
128                    165                     170                 175
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130    CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC      1115
131    Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
132                    180                     185                 190
133
134    CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC      1163
135    His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
136                    195                     200                 205
137
138    TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG      1211
139    Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
140            210                     215                 220
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142    AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG      1259
143    Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
144    225                     230                     235                 240
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146    CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC      1307
147    Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
148                    245                     250                 255
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150    AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG      1355
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INPUT SET: S25543.raw

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157
158   TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC      1451
159   Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
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162   AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC      1499
163   Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
164   305                 310                 315                 320
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166   GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA      1547
167   Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
168                   325                 330                 335
169
170   TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC      1595
171   Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
172               340                 345                 350
173
174   GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC      1643
175   Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
176           355                 360                 365
177
178   ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG      1691
179   Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
180           370                 375                 380
181
182   AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA      1739
183   Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
184   385                 390                 395                 400
185
186   CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC      1787
187   Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
188                   405                 410                 415
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190   AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC      1835
191   Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
192               420                 425                 430
193
194   ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG      1883
195   Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
196           435                 440                 445
197
198   GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA      1931
199   Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
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202   TCA TAGCTGCATT AAAAAAATAC AATATGGACA TGTAAAAAGA CAAAAACCAA           1984
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205
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206 GTTATCTGTT TCCTGTTCTC TTGTATAGCT GAAATTCCAG TTTAGGAGCT CAGTTGAGAA   2044
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208 ACAGTTCCAT TCAACTGGAA CATTTTTTTT TTTNCCTTTT AAGAAAGCTT CTTGTGATCC   2104
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210 TTNGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC AAACTCAGAA GGCTTTGGGA   2164
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212 TATGCTGTAT TTTAAAGGGA CAGTTTGTAA CTTGGGCTGT AAAGCAAACT GGGGCTGTGT   2224
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214 TTTCGATGAT GATGATNATC ATGATNATGA TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   2284
215
216 NNNNNNNNNN GATTTTAACA GTTTTACTTC TGGCCTTTCC TAGCTAGAGA AGGAGTTAAT   2344
217
218 ATTTCTAAGG TAACTCCCAT ATCTCCTTTA ATGACATTGA TTTCTAATGA TATAAATTTC   2404
219
220 AGCCTACATT GATGCCAAGC TTTTTTGCCA CAAAGAAGAT TCTTACCAAG AGTGGGCTTT   2464
221
222 GTGGAAACAG CTGGTACTGA TGTTCACCTT TATATATGTA CTAGCATTTT CCACGCTGAT   2524
223
224 GTTTATGTAC TGTAAACAGT TCTGCACTCT TGTACAAAAG AAAA   2568
225
226
227 (2) INFORMATION FOR SEQ ID NO:2:
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229   (i) SEQUENCE CHARACTERISTICS:
230   (A) LENGTH: 465 amino acids
231   (B) TYPE: amino acid
232   (D) TOPOLOGY: linear
233
234   (ii) MOLECULE TYPE: protein
235
236   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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238 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
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240
241 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
242   20   25   30
243
244 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
245   35   40   45
246
247 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
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250 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
251   65   70   75   80
252
253 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
254   85   90   95
255
256 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
257   100   105   110
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   US/08/866,354

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